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Human Plasma Metabolites Associated with Established AMD Risk Genes

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Financial Disclosures

I have no financial disclosures or conflicts of interest related to the content of this presentation

Summary

- AMD risk SNPs have an impact on the plasma metabolome
- Genetic-metabolomic associations can provide unique insights into the pathogenesis of AMD
- Highest number of associations were seen with ***LIPC* polymorphisms**, which were associated with **glycerophospholipid metabolites**
- ***LIPC* gene and glycerophospholipids pathway are likely crucial in AMD pathogenesis** and may represent potential targets for treatment of AMD

AMD

**Functional
consequences?**

34 loci

>7,000 SNPs

(single nucleotide
polymorphisms)

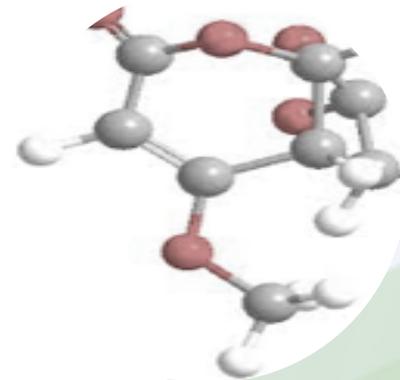
**Environmental
risk factors**

**Genetic
risk factors**

AMD



Genetic

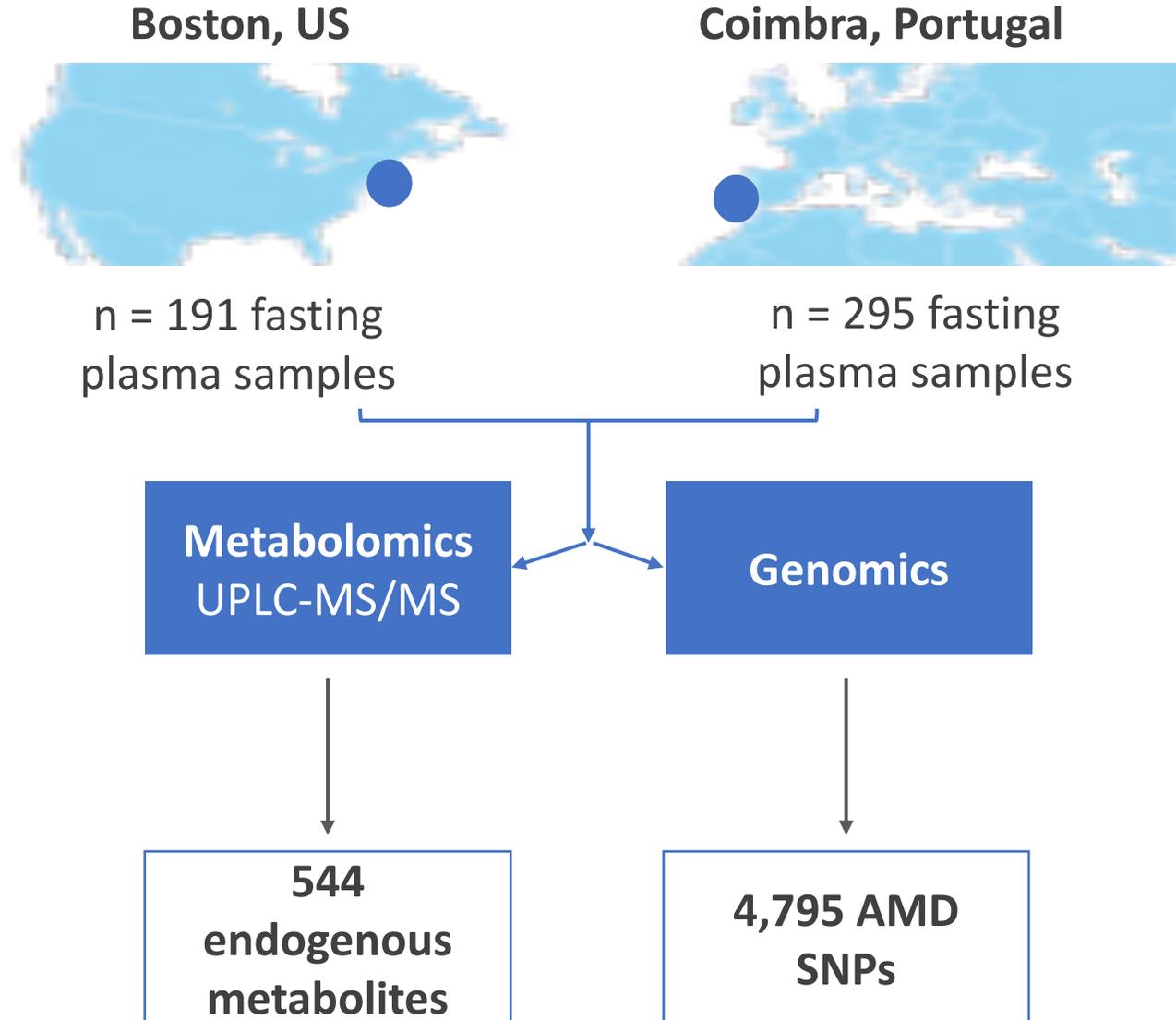


Metabolites

Goal

To analyze **associations between known AMD risk SNPs and plasma metabolites** in a cohort of AMD patients and controls

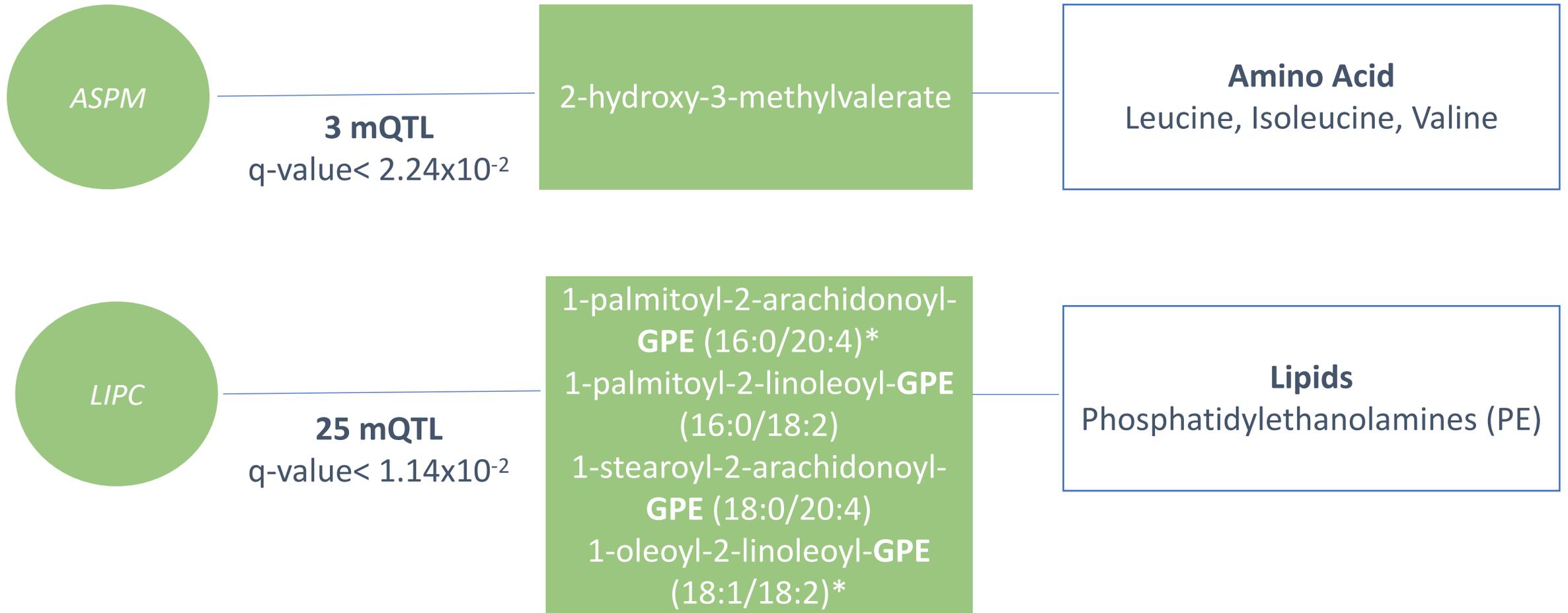
Methods



Methods

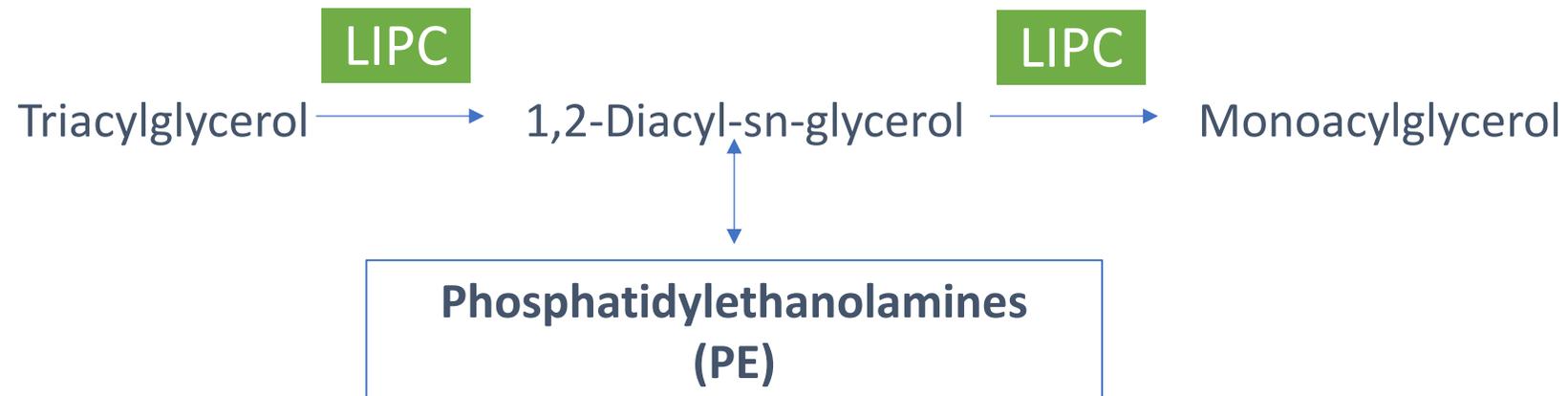
- Association between known AMD SNPs and plasma metabolites
 - Linear regression models adjusted for age, sex, smoking, 10 metabolite principal components (PCs) and 10 SNP PCs and accounting for false discovery rate
 - First for each cohort and then combined by meta-analysis

Results



Discussion

- *LIPC* gene with highest number of highly significant mQTL



Limitations

- Relatively small sample size
- Cross-sectional design

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Acknowledgments

- **Deeba Husain**

- **Joan W. Miller**

- Shujian Zhu
- Wonil Chung
- Qunyian Yuan Q
- Rachel S. Kelly
- Archana Nigalye
- Raviv Katz
- John B. Miller
- Ivana K. Kim
- Rufino Silva
- Demetrios G. Vavvas
- Jessica Lasky-Su
- Liming Liang

Funding

- Miller Retina Research Fund (Mass. Eye and Ear)
- Champalimaud Vision Award (JWM)
- Unrestricted Departmental Grant from Research to Prevent Blindness, Inc. New York
- Portuguese Foundation for Science and Technology / Harvard Medical School Portugal Program (HMSP-ICJ/006/2013)
- Commonwealth unrestricted grant for eye research



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Thank you!

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